# Expanded View Figures

**A**

*phyb-9 GI::LUC*

**B**

Simulated *PRR9*/*PRR7*
$L_{sens} = 0$; $J_{local} = 2$



**C**

*phyb-9 GI::LUC*

**E**

*phyb-9 GI::LUC*



**D**

Simulated *PRR9*/*PRR7*;
$L_{sens} = 0$; $J_{local} = 2$

**F**

Simulated *PRR9*/*PRR7*;
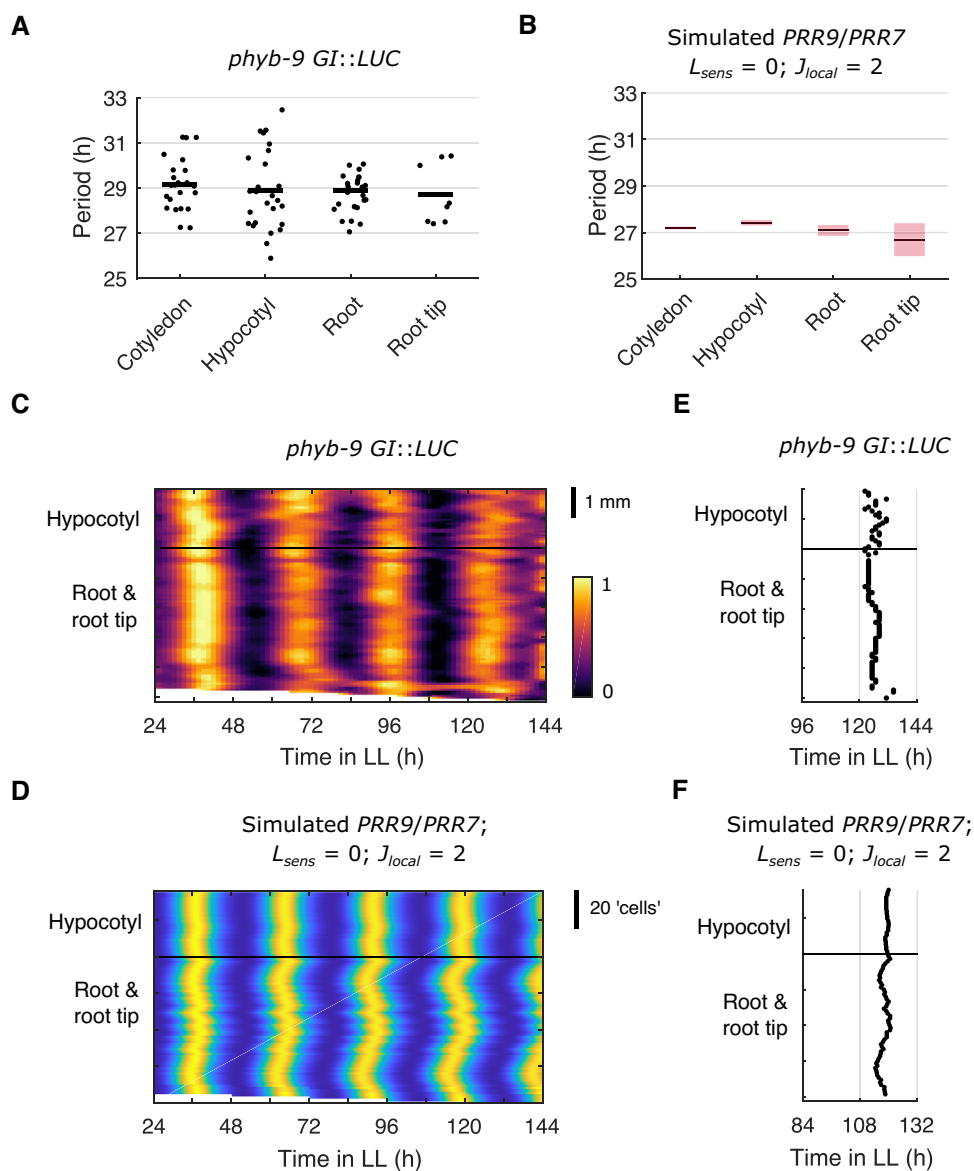$L_{sens} = 0$; $J_{local} = 2$



**Figure EV1. Simulations with zero light input capture the loss of period differences observed in the *phyb-9* mutant.**

A   Period estimates of *GI::LUC* expression measured from different organs under red light in the light-sensing mutant *phyb-9* genetic background. Each data point represents a period estimate from the organ of a single seedling and the horizontal black line shows the mean.

B   Period estimates of simulated *PRR9*/*PRR7* expression, measured from regions within the template seedling. Simulations were performed with zero light sensitivity for all cells ($L_{sens} = 0$; $D = 1$) and with local cell-to-cell coupling ($J_{local} = 2$). The horizontal black line shows the mean and the red shaded area one SD of 9 simulations.

C   Representative intensity plot of *GI::LUC* expression across longitudinal sections of a single seedling under constant red light. Imaging was performed under red light in the light-sensing mutant *phyb-9* genetic background.

D   Representative intensity plot of simulated *PRR9*/*PRR7* expression across longitudinal sections of a single seedling under LL. Simulations were performed with zero light sensitivity for all cells ($L_{sens} = 0$; $D = 1$) and with local cell-to-cell coupling ($J_{local} = 2$).

E, F   Times of the final peaks of *GI::LUC* intensity plot (E) or simulated *PRR9*/*PRR7* expression (F). Simulations were performed with zero light sensitivity for all cells ($L_{sens} = 0$; $D = 1$) and with local cell-to-cell coupling ($J_{local} = 2$).

Data information: Experimental data is an analysis of *Arabidopsis* time-lapse movies carried out previously (Greenwood *et al*, 2019). $N = 2$ and $n = 8$–23, where $N$ represents the number of independent experiments and $n$ the total number of organs tracked.
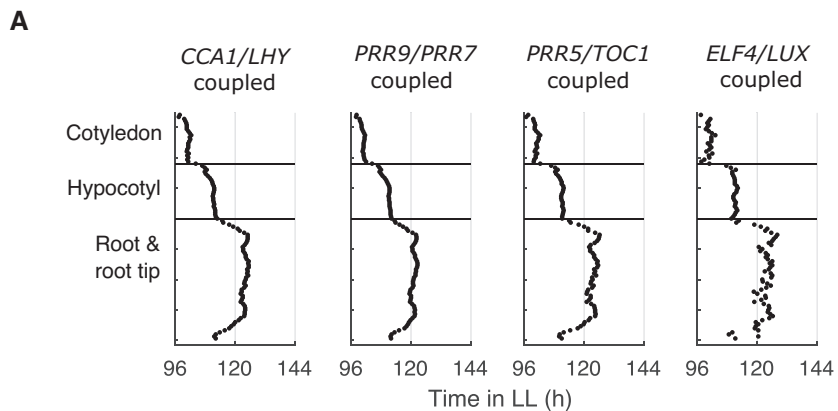
**A**



**B**



**Figure EV2.  Peaks of simulated expression with the local sharing of different clock molecules between cells.**

A, B  The times of the final peaks of simulated *PRR9/PRR7* intensity plots, simulated with the sharing of *CCA1/LHY*, *PRR9/PRR7*, *PRR5/TOC1*, or *ELF4/LUX* mRNA (A) or protein (B) locally between neighbor cells. Simulations were performed under LL with local cell-to-cell coupling ($J_{local}$ = 2).

Data information: Data in (A) ("*CCA1/LHY* coupled") is replotted from Fig 3D and data in (B) ("ELF4/LUX coupled") is replotted from Fig 4B.
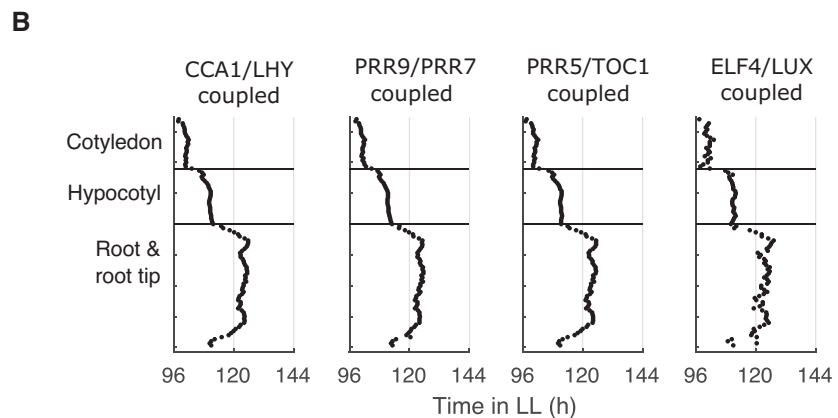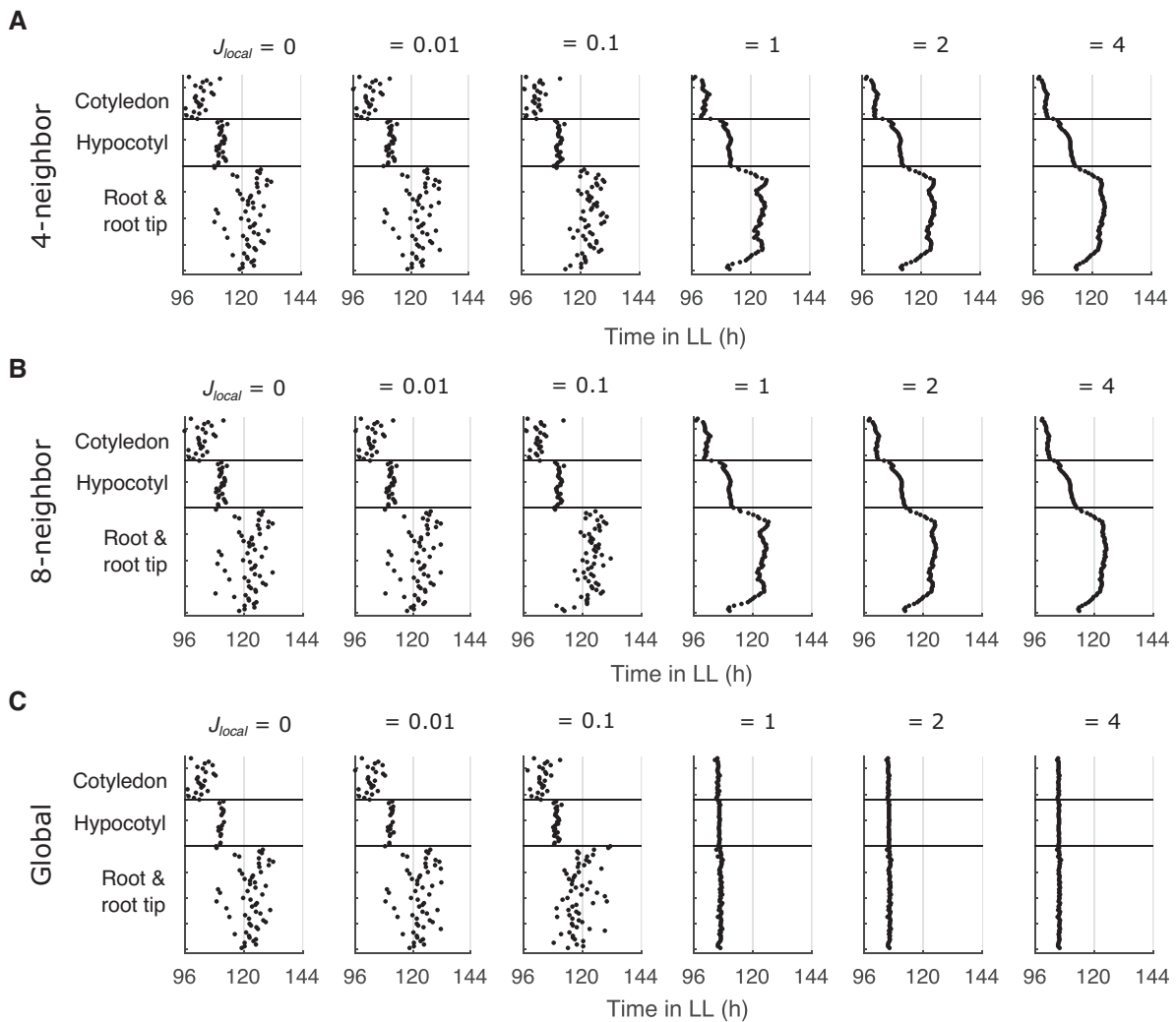
**Figure EV3. Peaks of simulated expression under LL with different coupling rules.**

A–C   The times of the final peaks of simulated *PRR9/PRR7* intensity plots, simulated under LL with increasing strengths of local cell-to-cell coupling between the 4 nearest neighbor cells (A), 8 nearest neighbor cells (B), or globally (all-to-all; C).

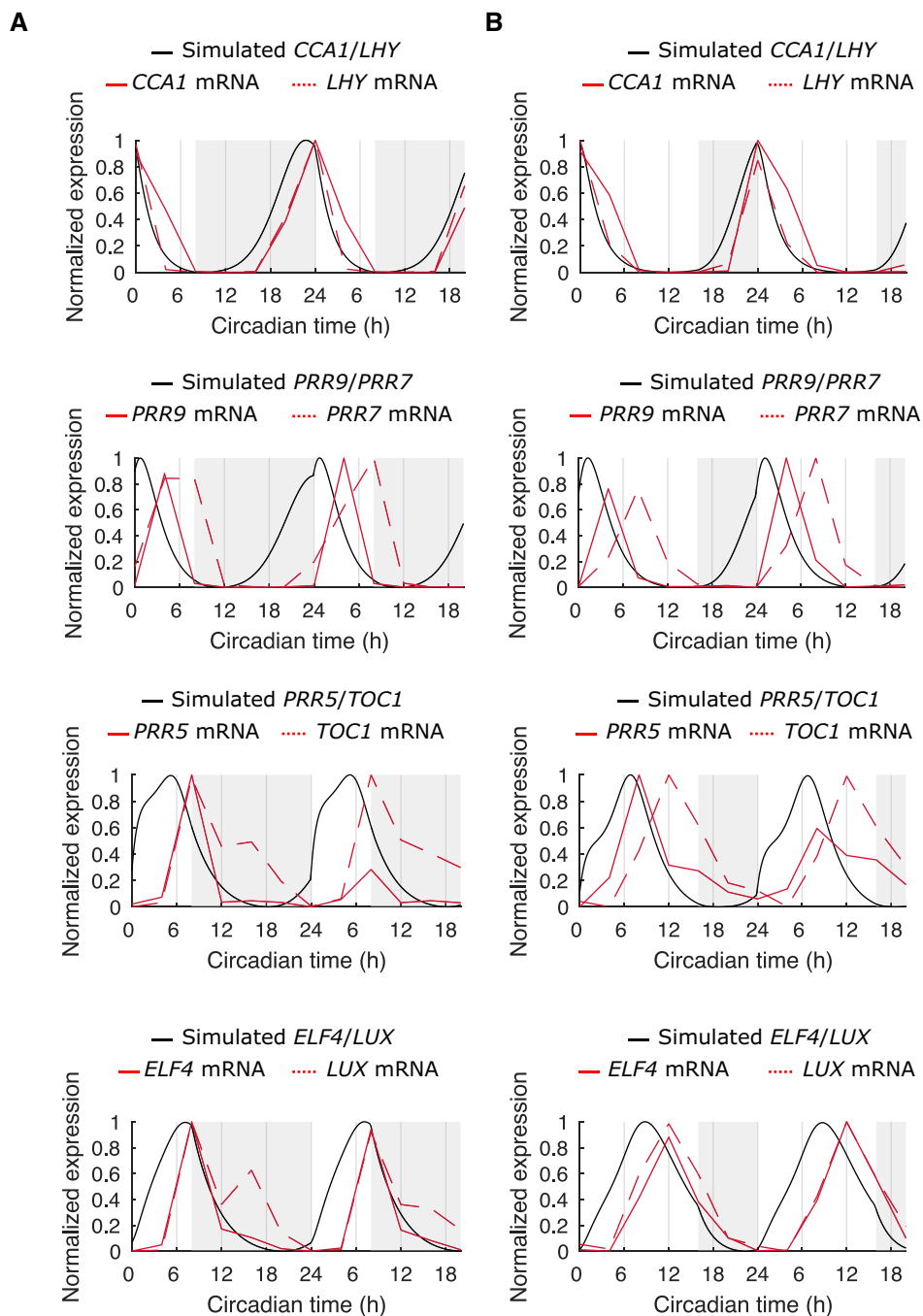Data information: (A) is replotted from Fig 3E.

**Figure EV4. Simulations under short- and long-day lengths approximate experimental data.**

A, B    Simulated (black line) and experimental (red line) expression of clock genes under idealized LD cycles with 8 h (A) or 16 h (B) day lengths. Simulations were
            implemented as a single cell, without variation in gene expression, and with $L_{sens}$ = 1.

Data information: Experimental data are *Arabidopsis* whole-plant averages obtained from the DIURNAL database (Mockler *et al*, 2007).